

FIG. 1

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SEQ ID NO: 1	-	ATGGCGGCGTCCTCCCTGGAAACAGAAAGCTGTCCCGCTGGAAAGCAAGCT	50
SEQ ID NO: 2	-	MetAlaAlaSerSerLeuGluGlnLvsLeuSerAraLeuGluAlaLvsLe	17
SEQ ID NO: 1	-	GAAGCAGGAGAACCGGGAGGCCCGCGGAGGATCGACCTCAACCTGGATA	100
SEQ ID NO: 2	-	uLysGlnGluAsnArgGluAlaArgArgArgIleAspLeuAsnLeuAspI	34
SEQ ID NO: 1	-	TCAGCCCCCAGCGGCCAGGCCCATTTATTGTGATCACTCTAAGCCCTGCT	150
SEQ ID NO: 2	-	leSerProGlnArgProArgProIleIleValIleThrLeuSerProAla	50
SEQ ID NO: 1	-	CCTGCCCCCGTCCCAACGAGCAGCCCTGCAGCTCCCGCTGGCCCAACGATGG	200
SEQ ID NO: 2	-	ProAlaProSerGlnArgAlaAlaLeuGlnLeuProLeuAlaAsnAspGl	67
SEQ ID NO: 1	-	GGCAGCCGCTCGCCATCCTCAGAGAGCTCCCCGCAGCACCCACGCCCC	250
SEQ ID NO: 2	-	yGlySerArgSerProSerSerGluSerSerProGlnHisProThrProp	84
SEQ ID NO: 1	-	CCGCCCGGCCCCACATGCTGGGGCTCCCGTCAACCCGTTCACACCC	300
SEQ ID NO: 2	-	roAlaArgProArgHisMetLeuGlyLeuProSerThrLeuPheThrPro	100
SEQ ID NO: 1	-	CGCAGCATGGAGAGCATTGAGATTGACCAGAAAGCTGCAGGAGATCATGAA	350
SEQ ID NO: 2	-	ArgSerMetGluSerIleGluIleAspGlnLysLeuGlnGluIleMetLy	117

FIG. 1
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SEQ ID NO: 1	- GCAGACGGGCTACCCGACCATCGGGGCCAGCGCTACCGAGCAGAAATCA	400
SEQ ID NO: 2	- sGlnThrGlyTyrProThrIleGlyGlyGlnArgTyrGlnAlaGluIleA	134
SEQ ID NO: 1	- ACGACCTGGAGAACTTGGGCGAGATGGGCAGCGGCACCTGCGGCCAGGTG	450
SEQ ID NO: 2	- snAspLeuGluAsnLeuGlyGluMetGlySerGlyThrCysGlyGlnVal	150
SEQ ID NO: 1	- TGGAAGATGCGCTTCCGGAAGACCGGCCACGTCAATTGCCGTTAAGCAAAT	500
SEQ ID NO: 2	- TrpLysMetArgPheArgLysThrGlyHisValIleAlaValLysGlnMe	167
SEQ ID NO: 1	- GCGGCGTCCGGGAACAAGGAGAGAAACAAGCGCATCCTCATGGACCTGG	550
SEQ ID NO: 2	- tArgArgSerGlyAsnLysGluGluAsnLysArgIleLeuMetAspLeuA	184
SEQ ID NO: 1	- ATGTGTGCTGAAGAGCCACGACTGCCCCCTACATCGTGCAGTGTGGG	600
SEQ ID NO: 2	- spValValLeuLysSerHisAspCysProTyrIleValGlnCysPheGly	200
SEQ ID NO: 1	- ACGTTCATCACCAACACGGACGCTCTTCATCGCCATGGAGCTCATGGGCAC	650
SEQ ID NO: 2	- ThrPheIleThrAsnThrAspValPheIleAlaMetGluLeuMetGlyTh	217
SEQ ID NO: 1	- CTGCGCTGAGAAAGCTCAAGAAGCGGATGCAGGGCCCCCATCCCCGAGCGCA	700
SEQ ID NO: 2	- rCysAlaGluLysLeuLysLysArgMetGlnGlyProIleProGluArgI	234

FIG. 1
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SEQ ID NO: 1	-	TTCTGGGCAAGATGACAGTGGCGATTGTGAAGGCGCTGTACTACCTGAAA	750
SEQ ID NO: 2	-	leLeuGlyLysMetThrValAlaIleValLysAlaLeuTyrTyrLeuLys	250
SEQ ID NO: 1	-	GAGAAGCACGGTGTCAATCCACCGCAGCGTCAAGCCCTCCAACATCCTGCT	800
SEQ ID NO: 2	-	GluLysHisGlyValIleHisArgAspValLysProSerAsnIleLeuLe	267
SEQ ID NO: 1	-	GGACGAGCGGGGCCAGATCAAGCTCTGCGACTTCGGCATCAGCGCGCGCC	850
SEQ ID NO: 2	-	uAspGluArgGlyGlnIleLysLeuCysAspPheGlyIleSerGlyArgL	284
SEQ ID NO: 1	-	TGGTGGACTCCAAGCCAAAGACGCGGAGCGCGGCTGTGCCGCTACATG	900
SEQ ID NO: 2	-	euValAspSerLysAlaLysThrArgSerAlaGlyCysAlaAlaTyrMet	300
SEQ ID NO: 1	-	GCACCCGAGCGCATTTGACCCCCCAGACCCCAAGCCGGACTATGACAT	950
SEQ ID NO: 2	-	AlaProGluArgIleAspProProAspProThrLysProAspTyrAspI	317
SEQ ID NO: 1	-	CCGGGCCGACGTATGGAGCCTGGGCATCTCGTTGGTGGAGCTGGCAACAG	1000
SEQ ID NO: 2	-	eArgAlaAspValTrpSerLeuGlyIleSerLeuValGluLeuAlaThrG	334
SEQ ID NO: 1	-	GACAGTTTCCCTACAAGAACTGCAAGACGGACTTTGAGGTCCTCACCAA	1050
SEQ ID NO: 2	-	lyGlnPheProTyrLysAsnCysLysThrAspPheGluValLeuThrLys	350

FIG. 1

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SEQ ID NO: 1 - GTCCTACAGGAAGCCCCCGCTTCTGCCCCGGACACATGGGCTTCTCGGG 1100
|||||
SEQ ID NO: 2 - ValLeuGlnGluGluProProLeuLeuProGlyHisMetGlyPheSerG1 367
|||||

SEQ ID NO: 1 - GGACTTCCAGTCCTTCGTCAAAGACTGCCTTACTAAAGATCACAGGAAGA 1150
|||||
SEQ ID NO: 2 - yAspPheGlnSerPheValLysAspCysLeuThrLysAspHisArgLysA 384
|||||

SEQ ID NO: 1 - GACCAAAGTATAATAAGCTACTTGAACACACAGCTTCAAGCGCTACGAG 1200
|||||
SEQ ID NO: 2 - rgProLysTyrAsnLysLeuLeuGluHisSerPheIleLysArgTyrGlu 400
|||||

SEQ ID NO: 1 - ACGCTGGAGGTGGACGTGGCGTCCCTGGTTCAAGGATGTCAATGGCGAAGAC 1250
|||||
SEQ ID NO: 2 - ThrLeuGluValAspValAlaSerTrpPheLysAspValMetAlaLysTh 417
|||||

SEQ ID NO: 1 - TGAGTCACCGCGGACTAGCGGCGTCCCTGAGCCAGCCCCACCTGCCCTTCTTCAGGTAG 1308
|||||
SEQ ID NO: 2 - rGluSerProArgThrSerGlyValLeuSerGlnProHisLeuProPhePheArgStop 435
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FIG. 2

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*      20      *      *      *      *      *
: ATGGCGCGTCCCTCGAAACAGAAAGCTGTCCCGCCTGGAAGCAAAAGCTGAAGCAGGAGAACCGGGAGGCCCGGC : 76
: ATGGCGCGTCCCTCGAGCAGAAAGCTGTCCCGCCTGGAAGCAAGCTGAAGCAGGAGAACCCGTAGGCCCGCA : 76

80      *      100      *      120      *      140      *
: GGAGGATCGACCTCAACCTGGATATCAGCCCCCAGCGGGCCCCAGGCCCATTTATTGTGATCACTCTAAGCCCCTGCTCC : 152
: GGAGGATCGACCTCAACTTGGATATCAGCCCCACAGCGGGCCCCAGGCCCATTTATTGTGATCACTCTAAGCCCCTGCTCC : 152

160      *      180      *      200      *      220
: TGCCCCGTCCCAACGAGCAGCCCTGCAGCTCCCGCTGGCCAAACGATGGGGGCAGCCGCTCGCCATCCTCAGAGAGC : 228
: TGCCCCGTCCAGCGAGCAGCCCTGCAACTCCCACCTGGCCAAACGATGGGGGCAGCCGCTCACCATCCTCAGAGAGC : 228

*      240      *      260      *      280      *      300
: TCCCCGCAGCACCACGCCCCCGCCCGCCACATGCTGGGGCTCCCCGTCAACCCCTGTTCAACACCCCGCA : 304
: TCCCCACAGCACCCTACACCCCCACCCGCCCGCCACATGCTGGGGCTCCCCATCAACCTTGTTCAACACCCGCA : 304

*      320      *      340      *      360      *      380
: GCATGGAGAGCATTGAGATTGACCAGAAAGCTGCAGGAGATCATGAAGCAGACGGGCTACCCGACCATCGGGGGGCA : 380
: GTATGGAGAGCATCGAGATTGACCAGAAAGCTGCAGGAGATCATGAAGCAGACAGGGTACCTGACTATCGGGGGCA : 380

*      400      *      420      *      440      *
: GCGTACCAGGCAGAAATCAACGACCTGGAGAACTTGGGCGGAGATGGGCAGCGGCACCTGCGGCCAGGTGTGGAAG : 456
: GCGTTATCAGGCAGAAATCAATGACTTGGAGAACTTGGGTGAGATGGGCAGTGGTACCTGTGTCAGGTGTGGAAG : 456

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FIG. 2

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460      *      480      500      520      *
: ATGCGCTTCCGGAAGACCGGCACGTCATTGCCGTTAAGCAAATGCGGCGCTCCGGGAACAAGGAGAGAACAAGC : 532
: ATGCGGTTCCGGAAGACAGGCCACATCATTTGCTGTTAAGCAAATGCGGCGCTCTGGGAACAAGGAAGATAAGC : 532

540      *      560      580      *      600
: GCATCCTCATGGACCTGGATGTGGTGTGAAGAGCCACGACTGCCCCCTACATCGTGCAGTGCTTTGGGACGTTTCAT : 608
: GCATTTTGATGGACCTGGATGTAGTACTCAAGAGCCATGACTGCCCTTACATCGTTCAAGTGCTTTGGCACCTTCAT : 608

*      620      *      640      *      660      *      680
: CACCAACACGACGCTTTCATCGCCATGGAGCTCATGGGCACCTGCGCTGAGAAGCTCAAGAAGCGGATGCAGGGC : 684
: CACCAACACAGACGCTTTTATTGCCCATGGAGCTCATGGGCACATGTGCAGAGAAGCTGAAGAAACGAATGCAGGGC : 684

*      700      *      720      *      740      *      760
: CCCATCCCCGAGCGCATTTCTGGGCAAGATGACAGTGGCGATTGTGAAGGCGCTGTACTACCTGAAGAGAACACG : 760
: CCCATTCCAGAGCGAATCCTGGGCAAGATGACTGTGGCGATTGTGAAGCACACTGTACTATCTGAAGGAGAAGCATG : 760

*      780,      *      800      *      820      *
: GTGTCATCCACCGGACGTCKAGCCCTCCAACATCCTGTGCTGGACGAGCGGGGCCAGATCAAGCTCTGCGACTTCGG : 836
: GCGTCATCCATCGCGATGTCAAACCCCTCCAACATCCTGTCTAGATGAGCGGGGCCAGATCAAGCTCTGTGACTTTGG : 836

840      *      860      *      880      *      900      *
: CATCAGCGGCCGCTGGTGGACTCCAAAGCCAAAGCGGAGCGCGGCTGTGCCGCCCTACATGGCACCCGAGCGC : 912
: CATCAGTGGCCGCTTGTTGACTCCAAAGCCAAACACGAGTGCTGGCTGTGCTGCCCTATATGGCTCCCCGAGCGC : 912

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FIG. 2

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920      *      940      960      *      980
: ATTGACCCCCAGACCCACCAAGCCGGACTATGACATCCGGGCCGACGTATGGAGCCTGGGCATCTCGTTGGTGG : 988
: ATCGACCCCTCCAGATCCCAAGCCTGACTATGACATCCGAGCTGATGTGTGGAGCCTGGGCATCTCACTGGTGG : 988

*      1000      *      1020      *      1040      *      1060
: AGCTGGCAACAGGACAGTTTCCCTACAAGAACTGCAAGACGGACTTTGAGGTCTCACCAAAGTCCCTACAGGAAGA : 1064
: AGCTGGCAACAGGACAGTTTCCCTATAAGAACTGCKAGACGGACTTTGAGGTCTCACCAAAGTCCCTACAGGAAGA : 1064

*      1080      *      1100      *      1120      *      1140
: GCCCCCGCTTCTGCCCCGACACATGGGCTTCTCGGGGGACTTCCAGTCCCTCGTCAAAGACTGCCCTTACTAAAGAT : 1140
: GCCCCCACTCCTGCCTGGTCACATGGGCTTCTCAGGGGACTTCCAGTCATTGTCAAAGACTGCCCTTACTAAAGAT : 1140

*      1160      *      1180      *      1200      *
: CACAGGAAGAGACCAAGTATAATAAGCTACTTGAACACACAGCTTCATCAAGCGCTACGAGACGCTGGAGGTGGACG : 1216
: CACAGGAAGAGACCAKAGTATAATAAGCTACTTGAACACACAGCTTCATCAAGCACTATGAGATACTCGAGGTGGATG : 1216

1220      *      1240      *      1260      *      1280      *
: TGGCGTCCCTGGTTCAAGGATGTTCATGGCGAAGACTGAGTCACCGCGGACTAGCGGCGTCTGAGCCAGCCCCACCT : 1292
: TCGCGTCCCTGGTTTAAGGATGTTCATGGCGAAGACCGAGTCCCCAAGGACTAGTGGAGTCCCTGAGTCAGCACCATCT : 1292

1300
: GCCCTTCTTCAGGTAG : 1308
: GCCCTTCTTCAGGTAG : 1308

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FIG. 3

SEQ ID NO: 2 - MAASSLEQKLSRLEAKLKQENREARRRRIDNLNDISPQRPRIIVITLSPAPAPSQRAALQ 60
|||||
SEQ ID NO: 12 - MAASSLEQKLSRLEAKLKQENREARRRRIDNLNDISPQRPRIIVITLSPAPAPSQRAALQ 60
|||||
SEQ ID NO: 2 - LPLANDGGSRSPSESSPQHPTPPARPRHMLGLPSTLFTPRSMESIEIDQKLQEIIMKQTG 120
|||||
SEQ ID NO: 12 - LPLANDGGSRSPSESSPQHPTPPTRPRHMLGLPSTLFTPRSMESIEIDQKLQEIIMKQTG 120
|||||
SEQ ID NO: 2 - YPTIGGQRYQAEINDLENLGEMSGTCCGQVWKMRFRKTGHVIAVKQMRRRSGNKEENKRIL 180
|||||
SEQ ID NO: 12 - YLTIGGQRYQAEINDLENLGEMSGTCCGQVWKMRFRKTGHIIIAVKQMRRRSGNKEENKRIL 180
|||||
SEQ ID NO: 2 - MDLDVVLKSHDCPYIVQCFTFITNTDVFIAEMLMGTCAEKLLKRMQGPPIPERILGKMTV 240
|||||
SEQ ID NO: 12 - MDLDVVLKSHDCPYIVQCFTFITNTDVFIAEMLMGTCAEKLLKRMQGPPIPERILGKMTV 240
|||||
SEQ ID NO: 2 - AIVKALYYLKEKHGVIHRDVKPSNILLDERGQIKLCDFGISGRLLVDSKAKTRAGCAAYM 300
|||||
SEQ ID NO: 12 - AIVKALYYLKEKHGVIHRDVKPSNILLDERGQIKLCDFGISGRLLVDSKAKTRAGCAAYM 300
|||||
SEQ ID NO: 2 - APERIDPPDPTKPDYDIRADVWSLGISLVELATGQFPYKNCKTDFEVLTKVLQEEPPLLP 360
|||||
SEQ ID NO: 12 - APERIDPPDPTKPDYDIRADVWSLGISLVELATGQFPYKNCKTDFEVLTKVLQEEPPLLP 360
|||||
SEQ ID NO: 2 - GHMGFSGDFQSFVKDCLTKDHRKRPKYNKLLLEHSFIKRYETLEVVDVASWFKDVMAKTESP 420
|||||
SEQ ID NO: 12 - GHMGFSGDFQSFVKDCLTKDHRKRPKYNKLLLEHSFIKHYEILEVDVASWFKDVMAKTESP 420
|||||
SEQ ID NO: 2 - RTSGVLSQPHLPFFR 435
|||||
SEQ ID NO: 12 - RTSGVLSQHHLPFFR 435
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